<u>Amendments to the Specification</u>

Please replace the Sequence Listing on pages 1-9 as filed on June 4, 2004, with a substitute Sequence Listing presented on pages 1-24, enclosed herewith.

On page 5, please replace the paragraph starting on line 27 with the following:

Fig. 1A-B. **Tat components of B. subtilis and E. coli.** The amino acid sequences of Tat components of B. subtilis and E. coli as deduced from the SubtiList (http://bioweb.pasteur.fr/Genolist/ SubtiList.html) and Colibri (http:/bioweb.pasteur.fr/ Genolist/Colibri.html) databases were used for comparisons. Identical amino acids, or conservative replacements are marked. Putative transmembrane segments, indicated in gray shading, were predicted with the TopPred2 algorithm (34, 35) **(A)** Comparison of TatAc (YnzA, SEQ ID NO:5), TatAd (YczB, SEQ ID NO:4) and TatAy (YdiI, SEQ ID NO:3) of B. subtilis (Bsu) with TatA (SEQ ID NO:1), TatB (SEQ ID NO:6) and TatE of E. coli (Eco) (SEQ ID NO: 2 1 6). **(B)** Comparison of TatCd (YcbT, SEQ ID NO:9) and TatCy (YdiJ, SEQ ID NO:8) of B. subtilis with TatC of E. coli (SEQ ID NO: 7[[-9]]).

On page 7, please replace the paragraph starting on line 14 with the following:

Fig 7. **Predicted twin-arginine (RR-)signal peptides of B. subtilis.** The listed signal peptides contain, in addition to the twin-arginines, at least one other residue of the consensus sequence (R-R-X-ΦΦ; printed in bold). The number of residues in the N- and H-domains of each signal peptide, and the average hydrophobicity (h) of each of these domains, as determined by the algorithms of Kyte and Doolittle (Kyte, J., and R. F. Doolittle [1982] A simple method for displaying the hydropathic character of a protein. J. Mol. Biol. 157:105-32), are indicated. Furthermore, the RR-motifs in the N-domain, and SPase I recognition sites in the C-domain (ie. positions -3 to -1 relative to the predicted SPase cleavage site) are shown. Proteins lacking a (putative) SPase I cleavage site, some of which contain additional transmembrane domains, are indicated with "TM". One protein containing cell wall binding repeats is indicated with "W".

Please replace Table I and the text following the Table, on page 56 with the following:

GC634-2 seqamd